

INPUT SET: S4268.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

3 (1) General Information:

MUKHERJEE, RANJAN

(ii) TITLE OF INVENTION:

Human Peroxisome Proliferator Activated Receptor γ

11 (iii) NUMBER OF SEQUENCES:

2

(iv) CORRESPONDENCE ADDRESS:

14
15 (A) ADDRESSEE: Lyon &
16 (B) STREET: 633 Wes
17
18 (C) CITY: Suite 4
19 (D) STATE: Los Ang
20 (E) COUNTRY: Califor
21 (F) ZIP: U.S.A.
90071-2

24 (v) COMPUTER READABLE FORM:

**3.5" Diskette, 1.44 Mb
storage
IBM Compatible
IBM P.C. DOS 5.0
Word Perfect 5.1**

33 (vi) CURRENT APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/380,051
36 (B) FILING DATE: January 30, 1995
37 (C) CLASSIFICATION:

40 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Warburg, Richard J.
43 (B) REGISTRATION NUMBER: 32,327
44 (C) REFERENCE/DOCKET NUMBER: 210/100

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47 (ix) TELECOMMUNICATION INFORMATION:

48
49 (A) TELEPHONE: (213) 489-1600
50 (B) TELEFAX: (213) 955-0440
51 (C) TELEX: 67-3510

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54

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56 (2) INFORMATION FOR SEQ ID NO: 1:

57

58 (i) SEQUENCE CHARACTERISTICS:

59

60 (A) LENGTH: 1641 base pairs
61 (B) TYPE: nucleic acid
62 (C) STRANDEDNESS: single
63 (D) TOPOLOGY: linear

64

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

66

67 GAATTCCGGA CCCTCAACAC CACTCCCTCT TAGCCAATAT TGTGCCTATT	50
68 GCCATACTAG TCTTTGCGCC TGCGAAGCAG CGGTGGCCTA GCCCTACTAG	100
70 TCTCAATCTC CAACATATAT CGGCCTAGAC TACGTACATA ACCTAAACCT	150
72 ACTCCAATGC TAAAACTAAT CGTCCCTTTT CTCAAACGAG AGTCAGCCTT	200
74 TAACGAAATG ACCATGGTTG ACACAGAGAT GCCATTCTGG CCCACCAACT	250
76 TTGGGATCAG CTCCGTGGAT CTCTCCGTAA TGGAAGACCA CTCCCACCTCC	300
78 TTTGATATCA AGCCCTTCAC TACTGTTGAC TTCTCCAGCA TTTCTACTCC	350
80 ACATTACGAA GACATTCCAT TCACAAGAAC AGATCCAGTG GTTGCAGATT	400
82 ACAAGTATGA CCTGAAACTT CAAGAGTACC AAAGTGCAAT CAAAGTGGAG	450
84 CCTGCATCTC CACCTTATTA TTCTGAGAAG ACTCAGCTCT ACAATAAGCC	500
86 TCATGAAGAG CCTTCCAACT CCCTCATGGC AATTGAATGT CGTGTCTGTG	550
88 GAGATAAACG TTCTGGATT CACTATGGAG TTCATGCTTG TGAAGGATGC	600
90 AAGGGTTTCT TCCGGAGAAC AATCAGATTG AAGCTTATCT ATGACAGATG	650
92 TGATCTAAC TGTCGGATCC ACAAAAAAG TAGAAATAAA TGTCAGTACT	700
94 GTCGGTTCA GAAATGCCTT GCAGTGGGGA TGTCTCATAA TGCCATCAGG	750
96 TTTGGGCGGA TGCCACAGGC CGAGAAGGAG AAGCTGTTGG CGGAGATCTC	800
98 CAGTGATATC GACCAGCTGA ATCCAGAGTC CGCTGACCTC CGGGCCCTGG	850

RAW SEQUENCE LISTING
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100 CAAAACATTT GTATGACTCA TACATAAAAGT CCTTCCCGCT GACCAAAGCA 900
101
102 AAGGCGAGGG CGATCTTGAC AGGAAAGACA ACAGACAAAT CACCATTCGT 950
103
104 TATCTATGAC ATGAATTCT TAATGATGGG AGAAGATAAA ATCAAGTTCA 1000
105
106 AACACATCAC CCCCCCTGCAG GAGCAGAGCA AAGAGGTGGC CATCCGCATC 1050
107
108 TTTCAAGGGCT GCCAGTTCG CTCCGTGGAG GCTGTGCAGG AGATCACAGA 1100
109
110 GTATGCCAAA AGCATTCCCTG GTTTGTAAA TCTTGACTTG AACGACCAAG 1150
111 TAACTCTCCT CAAATATGGA GTCCACGAGA TCATTTACAC AATGCTGGCC 1200
112
113 TCCTTGATGA ATAAAGATGG GGTTCTCATA TCCGAGGGCC AAGGCTTCAT 1250
114
115 GACAAGGGAG TTTCTAAAGA GCCTGCGAAA GCCTTTGGT GACTTTATGG 1300
116
117 AGCCCCAAGTT TGAGTTTGCT GTGAAGTTCA ATGCACTGGA ATTAGATGAC 1350
118
119 AGCGACTTGG CAATATTTAT TGCTGTCATT ATTCTCAGTG GAGACCGCCC 1400
120
121 AGGTTTGCTG AATGTGAAGC CCATTGAAGA CATTCAAGAC AACCTGCTAC 1450
122
123 AAGCCCTGGA GCTCCAGCTG AAGCTGAACC ACCCTGAGTC CTCACAGCTG 1500
124
125 TTTGCCAAGC TGCTCCAGAA AATGACAGAC CTCAGACAGA TTGTCACGGA 1550
126
127 ACACGTGCAG CTACTGCAGG TGATCAAGAA GACGGAGACA GACATGAGTC 1600
128
129 TTCACCCGCT CCTGCAGGAG ATCTACAAGG ACTTGTACTA G 1641
130
131
132
133
134
135

136 (2) INFORMATION FOR SEQ ID NO: 2:

137

138 (i) SEQUENCE CHARACTERISTICS:

139

140 (A) LENGTH: 494 amino acids
141 (B) TYPE: amino acid
142 (C) STRANDEDNESS: single
143 (D) TOPOLOGY: linear

144

145 (ii) MOLECULE TYPE: peptide

146

147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

148

149 Met Leu Lys Leu Ile Val Pro Phe Leu Lys Arg Glu Ser Ala Phe
150 5 10 15

151

152

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153 Asn Glu Met Thr Met Val Asp Thr Glu Met Pro Phe Trp Pro Thr
154 20 25 30
155
156 Asn Phe Gly Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His
157 35 40 45
158
159 Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser
160 50 55 60
161
162 Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe Thr Arg Thr
163 65 70 75
164
165 Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu Gln Glu
166 80 85 90
167
168 Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr Tyr
169 95 100 105
170
171 Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser
172 110 115 120
173
174 Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala
175 125 130 135
176
177 Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly
178 140 145 150
179
180 Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
181 155 160 165
182
183 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln
184 170 175 180
185
186 Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
187 185 190 195
188
189 Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu
190 200 205 210
191
192 Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser
193 215 220 225
194
195 Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile
196 230 235 240
197
198 Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr
199 245 250 255
200
201 Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn
202 260 265 270
203
204 Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr
205 275 280 285

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206
207 Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln
208 290 295 300
209
210 Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu
211 305 310 315
212
213 Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp
214 320 325 330
215
216 Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr
217 335 340 345
218
219 Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu
220 350 355 360
221
222 Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys
223 365 370 375
224 Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys
225 380 385 390
226
227 Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
228 395 400 405
229
230 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val
231 410 415 420
232
233 Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
234 425 430 435
235
236 Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala
237 440 445 450
238
239 Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu
240 455 460 465
241
242 His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met
243 470 475 480
244
245 Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
246 485 490

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**SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text